

Sequence Match Listing

RESULT 1
US-08-323-474-2
; Sequence 2, Application US/08323474
; Patent No. 5447860
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/323,474
; FILING DATE: 1992-06-26
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2609
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-323-474-2

Query Match 100.0%; Score 1708; DB 1; Length 1124;
Best Local Similarity 100.0%; Pred. No. 3e-155;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ALNRKVKNNDPDTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYA 60
Db 802 ALNRKVKNNDPDTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYA 861

Qy 61 SKDDHRDFAGELEVLCRKLGHHHPNIINLLGACEHRYLYLAIEYAPHGNLLDFLRKSRVLE 120
Db 862 SKDDHRDFAGELEVLCRKLGHHHPNIINLLGACEHRYLYLAIEYAPHGNLLDFLRKSRVLE 921
Qy 121 TDPAFAIANSTASTLSSQQLLHFADAVARGMDYLSQKQFIHRDLAARNILVGENYVAKIA 180
Db 922 TDPAFAIANSTASTLSSQQLLHFADAVARGMDYLSQKQFIHRDLAARNILVGENYVAKIA 981
Qy 181 DFGLSRGQEYVVKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCG 240
Db 982 DFGLSRGQEYVVKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCG 1041
Qy 241 MTCAELYEKLPQGYRLEKPLNCDDDEVYDLMRQCWRKPYERPSFAQILVSLNRMLEERKT 300
Db 1042 MTCAELYEKLPQGYRLEKPLNCDDDEVYDLMRQCWRKPYERPSFAQILVSLNRMLEERKT 1101
Qy 301 YVNNTTLYEKFTYAGIDCSAEEAA 323
Db 1102 YVNNTTLYEKFTYAGIDCSAEEAA 1124

Sequence Match Listing

RESULT 1
TIE2_HUMAN
ID TIE2_HUMAN STANDARD; PRT; 1124 AA.
AC Q02763;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEK) (P140 TEK) (Tunica interna endothelial cell kinase) (CD202b antigen).
GN TEK OR TIE2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93173509; PubMed=8382358;
RA Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R.;
RT "Molecular cloning and characterization of a novel receptor protein tyrosine kinase from human placenta.";
RL Oncogene 8:663-670(1993).
RN [2]
RP VARIANT VMCM1 TRP-849.
RX MEDLINE=97134665; PubMed=8980225;
RA Viikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J., Goumnerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C., Mulliken J.B., Olse B.R.;
RT "Vascular dysmorphogenesis caused by an activating mutation in the receptor tyrosine kinase TIE2.";
RL Cell 87:1181-1190(1996).
RN [3]
RP VARIANTS VMCM1 TRP-849 AND SER-897.
RX MEDLINE=99299243; PubMed=10369874;
RA Calvert J.T., Riney T.J., Kontos C.D., Cha E.H., Prieto V.G., Shea C.R., Berg J.N., Nevin N.C., Simpson S.A., Pasyk K.A., Speer M.C., Peters K.G., Marchuk D.A.;
RT "Allelic and locus heterogeneity in inherited venous malformations.";
RL Hum. Mol. Genet. 8:1279-1289(1999).
CC -!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL FORMATION.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN ENDOTHELIAL CELLS AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
CC -!- DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS MALFORMATIONS (VMCM1), AN ERROR OF VASCULAR MORPHOGENESIS CHARACTERIZED BY DILATED, SERPIGINOUS CHANNELS.

		SQ	SEQUENCE	1124 AA:	125810 MW:	65BC05D18FACCEC CRC64:
CC	-1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TIE					
CC	SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.					
CC	-1 SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.					
CC	-1 SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.					
CC	-1 DATABASE: NAME=PROB; NOTE=PROB 3.12-14(2002); WWW="http://www.ncbi.nlm.nih.gov/prob/guide/1715848914.g.htm"					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC	EMBL: L06139; AAA61139.1;					
DR	HSPB; P11352; IEGK..					
DR	GeneID: HGNC:11724; TEK.					
DR	MIM: 600221; .					
DR	MIM: 600195; .					
DR	InterPro: IPR000561; EGF-like.					
DR	InterPro: IPR00719; Eok_Pkinase.					
DR	InterPro: IPR00391; FN_III.					
DR	InterPro: IPR001245; TYR_Pkinase.					
DR	Pfam: PF00008; EGF; 1.					
DR	Pfam: PF00041; Fn3; 3.					
DR	Pfam: PF00069; Pkinase; 1.					
DR	PRINTS: PR00109; TYRKINASE.					
DR	ProDom: PD00001; Euk_Pkinase; 1.					
DR	SMART: SM00001; EGF_like; 1.					
DR	SMART: SM00060; Fn3; 3.					
DR	SMART: SM00219; TYRK; 1.					
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.					
DR	PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.					
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.					
DR	SMART: SM00001; EGF; 2.					
DR	PROSITE; PS0186; EGF_2; 3.					
KW	Receptor; Tyrosine protein kinase; Transferase; Signal; ATP-binding; Glycoprotein; Phosphorylation; Multigene family; Disease mutation.					
FT	SIGNAL 1 18 ANGIOTROPHIN 1 RECEPTOR.					
FT	CHAIN 19 745 EXTRACELLULAR (POTENTIAL).					
FT	DOMAIN 19 770 POTENTIAL.					
FT	TRANSMEM 746 1224 CYTOPLASMIC (POTENTIAL).					
FT	DOMAIN 771 102 IG-LIKE C2-TYPE DOMAIN 1.					
FT	DOMAIN 44 210 EGFR-LIKE 1.					
FT	DOMAIN 210 252 EGFR-LIKE 2.					
FT	DOMAIN 254 299 EGF-LIKE 3.					
FT	DOMAIN 301 341 IG-LIKE C2-TYPE DOMAIN 2.					
FT	DOMAIN 370 424 FIBRONECTIN TYPE-III 1.					
FT	DOMAIN 444 536 FIBRONECTIN TYPE-III 2.					
FT	DOMAIN 541 634 FIBRONECTIN TYPE-III 3.					
FT	DOMAIN 638 732 PROTEIN KINASE.					
FT	DOMAIN 824 1096 ATP (BY SIMILARITY).					
NP_BIND	830 838 ATP (BY SIMILARITY).					
BINDING	855 855 ATP (BY SIMILARITY).					
FT	ACT_SITE 964 964 BY SIMILARITY.					
FT	CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 399 399 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 438 438 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 596 596 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 649 649 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	CARBOHYD 691 691 N-LINKED (GLCNAC. .) (POTENTIAL).					
FT	MOD_RES 992 992 PHOSPHORYLATION (AUTO).					
FT	VARIANT 849 849 R -> W (IN VMCM1; ACTIVATING EFFECT).					
VARIANT	897 897 Y -> S (IN VMCM1; ACTIVATING EFFECT).					
	/FTid=VAR_008716.					